EXHIBIT "B"

| Home | Paracel BLAST Results | Help |

MEGABLAST 1.2.3-Paracel [2001-11-20]

Reference:
Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000),
"A greedy algorithm for aligning DNA sequences",
J Comput Biol 2000; 7(1-2):203-14.
Database: human_genome
           643 sequences; 200,654,690,654 total letters

Query= LEX 129 SEQ ID NO:1
           (3648 letters)

	Score	E
	(bits)	Value
Sequences producing significant alignments:		
chr10.25000001-30000000	2981	0.0

>chr10.25000001-30000000
           Length = 4999999

 Score = 2981 bits (1504), Expect = 0.0
 Identities = 1504/1504 (100%)
 Strand = Plus / Plus

```
Query: 2145    ggacgagctgaaaaaactctatgcccaactggaaatatataaaagaaagaagatgatcac 2204
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1036939 ggacgagctgaaaaaactctatgcccaactggaaatatataaaagaaagaagatgatcac
1036998


Query: 2205    aaacaacccccacctccagaaaaagcggtgctcgaagaagggcctaggtcgttccatcat 2264
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1036999 aaacaacccccacctccagaaaaagcggtgctcgaagaagggcctaggtcgttccatcat
1037058


Query: 2265    gagacgcattacggagatcccagagacagtcagccggcagtgctctaaagaggacaagga 2324
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1037059 gagacgcattacggagatcccagagacagtcagccggcagtgctctaaagaggacaagga
1037118


Query: 2325    gggcgccgaccatggcacagccaaaggcactgccctcatcaggaagaacccccagagtc 2384
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1037119 gggcgccgaccatggcacagccaaaggcactgccctcatcaggaagaacccccagagtc
1037178


Query: 2385    ttcagggaacacagggaaatccaaggaggagaccctgaaaaaccgagtcttctcactcaa 2444
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1037179 ttcagggaacacagggaaatccaaggaggagaccctgaaaaaccgagtcttctcactcaa
1037238
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Query: 2445     gaaatcccacagcacttatgaccacgtgagagaccaaacggaagagtccagtagcctacc 2504
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1037239  gaaatcccacagcacttatgaccacgtgagagaccaaacggaagagtccagtagcctacc
1037298


Query: 2505     cacagaaagccaagaggaggagacaacagaaaattccacactggaatccctgtcgggtaa 2564
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1037299  cacagaaagccaagaggaggagacaacagaaaattccacactggaatccctgtcgggtaa
1037358


Query: 2565     aaaactaacacaaaaactaaaagaagacagcgaggctgagtccacggagtcggtgccgtt 2624
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1037359  aaaactaacacaaaaactaaaagaagacagcgaggctgagtccacggagtcggtgccgtt
1037418


Query: 2625     ggtgtgcaagtcagcaagcgctcacaacctcagctcagagaagaaaactgggcacccacg 2684
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1037419  ggtgtgcaagtcagcaagcgctcacaacctcagctcagagaagaaaactgggcacccacg
1037478


Query: 2685     aacatcgatgttacagaagtctctcagtgtcatagcaagcgccaaggagaagactcttgg 2744
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1037479  aacatcgatgttacagaagtctctcagtgtcatagcaagcgccaaggagaagactcttgg
1037538


Query: 2745     attagctgggaaaacccaaacagcaggtgtggaagaacgcactaaatcccagaaaccttt 2804
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1037539  attagctgggaaaacccaaacagcaggtgtggaagaacgcactaaatcccagaaaccttt
1037598


Query: 2805     gccaaaagataaagagacaaacagaaatcactcaaattctgataacacagagactaaaga 2864
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1037599  gccaaaagataaagagacaaacagaaatcactcaaattctgataacacagagactaaaga
1037658


Query: 2865     tcctgcccccaaaactcaaatcctgcggaggagccaagaaagcctcagaaatctgggat 2924
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1037659  tcctgcccccaaaactcaaatcctgcggaggagccaagaaagcctcagaaatctgggat
1037718


Query: 2925     tatgaaacaacaaagggtcaaccccaccactgccaattctgacctgaacccaggcaccac 2984
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1037719  tatgaaacaacaaagggtcaaccccaccactgccaattctgacctgaacccaggcaccac
1037778


Query: 2985     ccagatgaaggacaactttgacattggggaggtgtgtccttgggaggtttatgacctgac 3044
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                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1037779   ccagatgaaggacaactttgacattggggaggtgtgtccttgggaggtttatgacctgac
1037838


Query: 3045      ccctggtcctgtgccttcagaatcaaaagttcaaaagcacgtatctattgtggcttctga 3104
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1037839   ccctggtcctgtgccttcagaatcaaaagttcaaaagcacgtatctattgtggcttctga
1037898


Query: 3105      aatggagaaaaaccccactttttccttaaaggagaaatctcaccacaagcctaaggcagc 3164
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1037899   aatggagaaaaaccccactttttccttaaaggagaaatctcaccacaagcctaaggcagc
1037958


Query: 3165      tgaggtttgtcagcaatccaatcagaagcgcatagataaggctgaagtatgcctttggga 3224
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1037959   tgaggtttgtcagcaatccaatcagaagcgcatagataaggctgaagtatgcctttggga
1038018


Query: 3225      gagccaaggccagtccattttggaagatgagaagcttttgatttccaagactccagttct 3284
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1038019   gagccaaggccagtccattttggaagatgagaagcttttgatttccaagactccagttct
1038078


Query: 3285      cccagagagggcaaaagaggagaacggaggtcagcctcgtgcagccaatgtgtgtgctgg 3344
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1038079   cccagagagggcaaaagaggagaacggaggtcagcctcgtgcagccaatgtgtgtgctgg
1038138


Query: 3345      gcagagcgaagaactgccccccaaagctgtagcatcaaaaacagagaatgaaaatctcaa 3404
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1038139   gcagagcgaagaactgccccccaaagctgtagcatcaaaaacagagaatgaaaatctcaa
1038198


Query: 3405      ccaaataggacaccaggaaaaaaagacatcttcttctgaggagaatgtgcgtggctccta 3464
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1038199   ccaaataggacaccaggaaaaaaagacatcttcttctgaggagaatgtgcgtggctccta
1038258


Query: 3465      taactcaagtaataacttccagcaacctttaacatcacgagcagaggtttgtccttggga 3524
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1038259   taactcaagtaataacttccagcaacctttaacatcacgagcagaggtttgtccttggga
1038318


Query: 3525      gtttgagaccccagctcaaccaaatgctggaagaagtgtagctttacctgcctcttctgc 3584
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1038319   gtttgagaccccagctcaaccaaatgctggaagaagtgtagctttacctgcctcttctgc
1038378
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Query: 3585      tctaagtgcaaataagatagcagggcctaggaaagaagagatctgggatagttttaaagt 3644
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1038379  tctaagtgcaaataagatagcagggcctaggaaagaagagatctgggatagttttaaagt
1038438


Query: 3645      gtag 3648
                 ||||
Sbjct: 1038439  gtag 1038442



 Score = 1790 bits (903), Expect = 0.0
 Identities = 903/903 (100%)
 Strand = Plus / Plus


Query: 1        atgggagccatggcttaccccttactcctctgcctcctgcttgctcagctgggattggga 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 614589   atgggagccatggcttaccccttactcctctgcctcctgcttgctcagctgggattggga 614648


Query: 61       gctgttggcgccagccgcgacccccaaggacggccggattcccctcgagagaggaccccg 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 614649   gctgttggcgccagccgcgacccccaaggacggccggattcccctcgagagaggaccccg 614708


Query: 121      aaggggaagccgcacgcccagcagccgggtcgagcctctgcctcggactcctcggctccc 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 614709   aaggggaagccgcacgcccagcagccgggtcgagcctctgcctcggactcctcggctccc 614768


Query: 181      tggagccgctccaccgatggcaccatcttggcgcagaaactcgccgaggaggtgcccatg 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 614769   tggagccgctccaccgatggcaccatcttggcgcagaaactcgccgaggaggtgcccatg 614828


Query: 241      gacgtggcctcttacctctacaccggggactcccaccagctgaagcgagccaactgctcc 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 614829   gacgtggcctcttacctctacaccggggactcccaccagctgaagcgagccaactgctcc 614888


Query: 301      ggccgctacgagttggcgggcctgccggggaagtggccagccctggccagcgcgcacccc 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 614889   ggccgctacgagttggcgggcctgccggggaagtggccagccctggccagcgcgcacccc 614948


Query: 361      tccttgcaccgggcgctggacacactgacacacgccaccaacttcctcaacgtgatgctg 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 614949   tccttgcaccgggcgctggacacactgacacacgccaccaacttcctcaacgtgatgctg 615008


Query: 421      cagagcaataagtcgcggggagcagaacttgcaggacgacctggattggtaccaggcgctg 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 615009   cagagcaataagtcgcggggagcagaacttgcaggacgacctggattggtaccaggcgctg 615068
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Query: 481      gtgtggagccttctggagggcgagcccagcatctcccgggcggccatcaccttcagcacc 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 615069   gtgtggagccttctggagggcgagcccagcatctcccgggcggccatcaccttcagcacc 615128


Query: 541      gattcgctgtccgcaccggccccacaggtcttcctccaggccacgcgcgaggagagccgc 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 615129   gattcgctgtccgcaccggccccacaggtcttcctccaggccacgcgcgaggagagccgc 615188


Query: 601      atcctgctccaagacctgtcctcctccgcaccccacctggccaacgccactctggagacc 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 615189   atcctgctccaagacctgtcctcctccgcaccccacctggccaacgccactctggagacc 615248


Query: 661      gagtggttccacggcctccggcgcaagtggaggccccacttacaccgccgcggccccaat 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 615249   gagtggttccacggcctccggcgcaagtggaggccccacttacaccgccgcggccccaat 615308


Query: 721      caggggccccggggcctgggccacagctggcggcgcaaggacgggctcggcggggacaag 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 615309   caggggccccggggcctgggccacagctggcggcgcaaggacgggctcggcggggacaag 615368


Query: 781      agccacttcaagtggtctccgccttatctggagtgcgagaacgggagttacaagcccggg 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 615369   agccacttcaagtggtctccgccttatctggagtgcgagaacgggagttacaagcccggg 615428


Query: 841      tggctggttactctttcctctgccatctacgggttgcagcctaacctggtcccggaattc 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 615429   tggctggttactctttcctctgccatctacgggttgcagcctaacctggtcccggaattc 615488


Query: 901      agg 903
                |||
Sbjct: 615489   agg 615491



 Score =  478 bits (241), Expect = e-131
 Identities = 241/241 (100%)
 Strand = Plus / Plus


Query: 1513     agggttttgaaggtgtttctttcacgaacggctcaacgaattccatatatgactggcgga 1572
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1011815  agggttttgaaggtgtttctttcacgaacggctcaacgaattccatatatgactggcgga
1011874


Query: 1573     cgggtcatgaggatgctggcagtaatactcttggtagtgttttggtttctcattggctgg 1632
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct: 1011875 cgggtcatgaggatgctggcagtaatactcttggtagtgttttggtttctcattggctgg
1011934


Query: 1633    acttcatctgtgtgccagaatttggagaaacagatttcacttattggccaggggaaaaca 1692
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1011935 acttcatctgtgtgccagaatttggagaaacagatttcacttattggccaggggaaaaca
1011994


Query: 1693    tccgatcacctcatcttcaatatgtgcctcattgaccgctgggactacatgacagcagtt 1752
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1011995 tccgatcacctcatcttcaatatgtgcctcattgaccgctgggactacatgacagcagtt
1012054


Query: 1753    g 1753
               |
Sbjct: 1012055 g 1012055



 Score =  438 bits (221), Expect = e-119
 Identities = 231/234 (98%), Gaps = 1/234 (0%)
 Strand = Plus / Plus


Query: 1102   aactttcggagaagggggtccggatcagcatatttcaggaagtacaaaagatgtgtcagaa 1161
              ||||||| | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 851409 aactttcag-gaagggggtccggatcagcatatttcaggaagtacaaaagatgtgtcagaa 851467


Query: 1162   gaagcctatgtctgcctaccttgcagggagggctgccccttctgtgctgatgacagccca 1221
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 851468 gaagcctatgtctgcctaccttgcagggagggctgccccttctgtgctgatgacagccca 851527


Query: 1222   tgcttcgtccaggaagataagtatttacgacttgccatcatctccttccaaggcctgtgt 1281
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct: 851528 tgcttcgtccaggaagataagtatttacgacttgccatcatctccttccaagccctgtgt 851587


Query: 1282   atgctgctcgacttcgttagcatgctggtggtctaccactttcgcaaagcaaag 1335
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 851588 atgctgctcgacttcgttagcatgctggtggtctaccactttcgcaaagcaaag 851641



 Score =  297 bits (150), Expect = 2e-77
 Identities = 150/150 (100%)
 Strand = Plus / Plus


Query: 1997    agttttcacattcaagcaataacccacgagatgatattgctacagaagcatatgaggatg 2056
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1035809 agttttcacattcaagcaataacccacgagatgatattgctacagaagcatatgaggatg
1035868
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Query: 2057    agctagacatgggccgatctggatcctacctgaacagcagtatcaattcagcctggagtg 2116
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1035869 agctagacatgggccgatctggatcctacctgaacagcagtatcaattcagcctggagtg
1035928


Query: 2117    agcacagcttggatccagaggacattcggg 2146
               ||||||||||||||||||||||||||||||
Sbjct: 1035929 agcacagcttggatccagaggacattcggg 1035958



 Score =  278 bits (140), Expect = 2e-71
 Identities = 140/140 (100%)
 Strand = Plus / Plus


Query: 1753    gctgaattttttattcctcttgtggggtgtttatctctgctatgcagtgcggacagtccca 1812
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1028174 gctgaattttttattcctcttgtggggtgtttatctctgctatgcagtgcggacagtccca
1028233


Query: 1813    tcggcattccatgagccccgctatatggctgttgcagttcacaatgagctcatcatctct 1872
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1028234 tcggcattccatgagccccgctatatggctgttgcagttcacaatgagctcatcatctct
1028293


Query: 1873    gctatattccatacaattag 1892
               ||||||||||||||||||||
Sbjct: 1028294 gctatattccatacaattag 1028313



 Score =  220 bits (111), Expect = 5e-54
 Identities = 111/111 (100%)
 Strand = Plus / Plus


Query: 1405    gttgttattttgtactttgagccaagcacatttcgctgtattctcctaagatgggctcgt 1464
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 990144  gttgttattttgtactttgagccaagcacatttcgctgtattctcctaagatgggctcgt 990203


Query: 1465    cttctcggttttgctactgtttacggaactgtcactctcaaacttcacagg 1515
               |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 990204  cttctcggttttgctactgtttacggaactgtcactctcaaacttcacagg 990254



 Score =  214 bits (108), Expect = 3e-52
 Identities = 108/108 (100%)
 Strand = Plus / Plus
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```
Query: 901      aggggtgtcatgaaagttgacataaatcttcagaaagtggacattgaccaatgctcaagt 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 660218  aggggtgtcatgaaagttgacataaatcttcagaaagtggacattgaccaatgctcaagt 660277


Query: 961      gatggctggttttcaggaactcataaatgccacctcaacaattcagag 1008
                ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 660278  gatggctggttttcaggaactcataaatgccacctcaacaattcagag 660325



 Score =  214 bits (108), Expect = 3e-52
 Identities = 108/108 (100%)
 Strand = Plus / Plus


Query: 1891     agatttgttcttgcctcaagacttcagtctgattggatgttgatgctgtattttgcacat 1950
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1033458  agatttgttcttgcctcaagacttcagtctgattggatgttgatgctgtattttgcacat
1033517


Query: 1951     actcatttgactgtgacagtcaccattgggttgcttttgattccaaag 1998
                ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1033518  actcatttgactgtgacagtcaccattgggttgcttttgattccaaag 1033565



 Score =  212 bits (107), Expect = 1e-51
 Identities = 110/111 (99%)
 Strand = Plus / Plus


Query: 1002     ttcagagtgtatgccaattaaaggcctaggattcgttcttggagcctatgagtgcatttg 1061
                ||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 835072   ttcatagtgtatgccaattaaaggcctaggattcgttcttggagcctatgagtgcatttg 835131


Query: 1062     caaagcaggattctatcatcctggagtcttaccagtgaacaactttcggag 1112
                |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 835132   caaagcaggattctatcatcctggagtcttaccagtgaacaactttcggag 835182



 Score =  145 bits (73), Expect = 2e-31
 Identities = 73/73 (100%)
 Strand = Plus / Plus


Query: 1334     agagcatccgggcatcgggccttatcctgttggaaacgatcctttttggatctctgctcc 1393
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 905817   agagcatccgggcatcgggccttatcctgttggaaacgatcctttttggatctctgctcc 905876


Query: 1394     tatactttccagt 1406
                |||||||||||||
```

Sbjct: 905877 tatactttccagt 905889

Database: mouse_genome
    Posted date: Jul 30, 2003 8:10 AM
Number of letters in database: 200,654,690,654
Number of sequences in database: 643

Lambda   K   H
   1.37   0.711   1.31

Gapped
Lambda   K   H
   1.37   0.711   1.31

Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 0, Extension: 0
Number of Hits to DB: 0
length of query: 7298
length of database: 200,654,690,654
effective HSP length: 22
effective length of query: 3626
effective search space used: 0
T: 0
A: 0
X1: 0 (0.0 bits)
X2: 20 (39.6 bits)
S1: 12 (24.3 bits)
S2: 24 (48.1 bits)